Please replace the paragraphs on page 44, lines 8-24 with the following paragraphs:

The glycosylation site was next removed by replacing the region from a unique *Xcm*I site to a unique *Sph*I site within the BPI gene in pSS101 with an annealed oligonucleotide that contained the codon (TCC) for the serine at amino acid position 351 changed to the codon (GCC) for alanine as shown below.

```
Wild type
     XcmI                                          SphI
...CCC AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC (SEQ ID NO:9)
...GGG TTC AGG AGG GAC CGA AGG GAG AAG GAC TAA CCG TAC GTG (SEQ ID NO:10)
   Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile GlyMet His (SEQ ID NO:11)
                351
Nonglycosylated
     XcmI                                          SphI
...CCC AAC TCC GCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC (SEQ ID NO:12)
...GGG TTC AGG CGG GAC CGA AGG GAG AAG GAC TAA CCG TAC GTG (SEQ ID NO:13)
   Pro Asn Ser Ala Leu Ala Ser Leu Phe Leu Ile Gly Met His (SEQ ID NO:14)
                351
```

This step generated the plasmid pSS102.

Amendments to the Claims

Please amend claims 1-2 and 22 so as to read as follows:

1. A method of three-dimensional modeling of a bactericidal/permeability-increasing ("BPI") protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising the step of using atomic coordinates of bactericidal/permeability-increasing ("BPI") protein, or fragment, analog or variant thereof, to generate a three-dimensional structural representation of the BPI protein.

2. A method of three-dimensional modeling of a bactericidal/permeability-increasing ("BPI") related lipid transfer protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising the step of using atomic coordinates of bactericidal/permeability-increasing ("BPI") protein, or fragment, analog or variant thereof, to generate a three-dimensional structural representation of the BPI-related lipid transfer protein.